



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- a1
- (i) APPLICANT: BARCHFELD, GAIL
DEL GIUDICE, GIUSEPPE
RAPPUOLI, RINO
 - (ii) TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
 - (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY -
R440
 - (B) STREET: P.O. BOX 8097
 - (C) CITY: EMERYVILLE
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: USA
 - (F) ZIP: 94662-8097
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/044,696
 - (B) FILING DATE: 18-MAR-1998
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/041,227
 - (B) FILING DATE: 21-MAR-1997
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HARBIN, ALISA A.
 - (B) REGISTRATION NUMBER: 33,895
 - (C) REFERENCE/DOCKET NUMBER: 1393.002
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (510) 655-8730
 - (B) TELEFAX: (510) 655-3542

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..708
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AUG 17 1998
GROUP 1

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AAT GGC GAC AGA TTA TAC CGT GCT GAC TCT AGA CCC CCA GAT GAA ATA	48
Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile	
1 5 10 15	
AAA CGT TTC CGG AGT CTT ATG CCC AGA GGT AAT GAG TAC TTC GAT AGA	96
Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg	
20 25 30	
GGA ACT CAA ATG AAT ATT AAT CTT TAT GAT CAC GCG AGA GGA ACA CAA	144
Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln	
35 40 45	
ACC GGC TTT GTC AGA TAT GAT GAC GGA TAT GTT TCC ACT TCT CTT AGT	192
Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser	
50 55 60	
TTG AGA AGT GCT CAC TTA GCA GGA CAG TAT ATA TTA TCA GGA TAT TCA	240
Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser	
65 70 75 80	
CTT ACT ATA TAT ATC GTT ATA GCA AAT ATG TTT AAT GTT AAT GAT GTA	288
Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val	
85 90 95	
ATT AGC GTA TAC AGC CCT CAC CCA TAT GAA CAG GAG GTT TCT GCG TTA	336
Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu	
100 105 110	
GGT GGA ATA CCA TAT TCT CAG ATA TAT GGA TGG TAT CGT GTT AAT TTT	384
Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe	
115 120 125	
GGT GTG ATT GAT GAA CGA TTA CAT CGT AAC AGG GAA TAT AGA GAC CGG	432
Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg	
130 135 140	
TAT TAC AGA AAT CTG AAT ATA GCT CCG GCA GAG GAT GGT TAC AGA TTA	480
Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu	
145 150 155 160	
GCA GGT TTC CCA CCG GAT CAC CAA GCT TGG AGA GAA GAA CCC TGG ATT	528
Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile	
165 170 175	
CAT CAT GCA CCA CAA GGT TGT GGA GAT TCA TCA AGA ACA ATC ACA GGT	576
His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly	
180 185 190	
GAT ACT TGT AAT GAG GAG ACC CAG AAT CTG AGC ACA ATA TAT CTC AGG	624
Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg	
195 200 205	
GAA TAT CAA TCA AAA GTT AAG AGG CAG ATA TTT TCA GAC TAT CAG TCA	672
Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser	
210 215 220	
GAG GTT GAC ATA TAT AAC AGA ATT CGG GAT GAA TTA TGA	711
Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu	
225 230 235	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
 1 5 10 15
 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
 20 25 30
 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
 35 40 45
 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
 50 55 60
 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
 65 70 75 80
 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
 85 90 95
 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
 100 105 110
 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
 115 120 125
 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
 130 135 140
 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
 145 150 155 160
 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
 165 170 175
 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
 180 185 190
 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
 195 200 205
 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
 210 215 220
 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAT GAT GAT AAG TTA TAT CGG GCA GAT TCT AGA CCT CCT GAT GAA ATA	48
Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile	
240 245 250	
AAG CAG TCA GGT GGT CTT ATG CCA AGA GGA CAG AGT GAG TAC TTT GAC	96
Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp	
255 260 265	
CGA GGT ACT CAA ATG AAT ATC AAC CTT TAT GAT CAT GCA AGA GGA ACT	144
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr	
270 275 280	
CAG ACG GGA TTT GTT AGG CAC GAT GAT GGA TAT GTT TCC ACC TCA ATT	192
Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile	
285 290 295 300	
AGT TTG AGA AGT GCC CAC TTA GTG GGT CAA ACT ATA TTG TCT GGT CAT	240
Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His	
305 310 315	
TCT ACT TAT TAT ATA TAT GTT ATA GCC ACT GCA CCC AAC ATG TTT AAC	288
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn	
320 325 330	
GTT AAT GAT GTA TTA GGG GCA TAC AGT CCT CAT CCA GAT GAA CAA GAA	336
Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu	
335 340 345	
GTT TCT GCT TTA GGT GGG ATT CCA TAC TCC CAA ATA TAT GGA TGG TAT	384
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr	
350 355 360	
CGA GTT CAT TTT GGG GTG CTT GAT GAA CAA TTA CAT CGT AAT AGG GGC	432
Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly	
365 370 375 380	
TAC AGA GAT AGA TAT TAC AGT AAC TTA GAT ATT GCT CCA GCA GCA GAT	480
Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp	
385 390 395	
GGT TAT GGA TTG GCA GGT TTC CCT CCG GAG CAT AGA GCT TGG AGG GAA	528
Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu	
400 405 410	
GAG CCG TGG ATT CAT CAT GCA CCG CCG GGT TGT GGG AAT GCT CCA AGA	576
Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg	
415 420 425	
TCA TCG ATC AGT AAT ACT TGC GAT GAA AAA ACC CAA AGT CTA GGT GTA	624
Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val	
430 435 440	
AAA TTC CTT GAC GAA TAC CAA TCT AAA GTT AAA AGA CAA ATA TTT TCA	672
Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser	
445 450 455 460	
GGC TAT CAA TCT GAT ATT GAT ACA CAT AAT AGA ATT AAG GAT GAA TTA	720
Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu	
465 470 475	
TGA	723

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn	Asp	Asp	Lys	Leu	Tyr	Arg	Ala	Asp	Ser	Arg	Pro	Pro	Asp	Glu	Ile	1	5	10	15
Lys	Gln	Ser	Gly	Gly	Leu	Met	Pro	Arg	Gly	Gln	Ser	Glu	Tyr	Phe	Asp	20	25	30	
Arg	Gly	Thr	Gln	Met	Asn	Ile	Asn	Leu	Tyr	Asp	His	Ala	Arg	Gly	Thr	35	40	45	
Gln	Thr	Gly	Phe	Val	Arg	His	Asp	Asp	Gly	Tyr	Val	Ser	Thr	Ser	Ile	50	55	60	
Ser	Leu	Arg	Ser	Ala	His	Leu	Val	Gly	Gln	Thr	Ile	Leu	Ser	Gly	His	65	70	75	80
Ser	Thr	Tyr	Tyr	Ile	Tyr	Val	Ile	Ala	Thr	Ala	Pro	Asn	Met	Phe	Asn	85	90	95	
Val	Asn	Asp	Val	Leu	Gly	Ala	Tyr	Ser	Pro	His	Pro	Asp	Glu	Gln	Glu	100	105	110	
Val	Ser	Ala	Leu	Gly	Gly	Ile	Pro	Tyr	Ser	Gln	Ile	Tyr	Gly	Trp	Tyr	115	120	125	
Arg	Val	His	Phe	Gly	Val	Leu	Asp	Glu	Gln	Leu	His	Arg	Asn	Arg	Gly	130	135	140	
Tyr	Arg	Asp	Arg	Tyr	Tyr	Ser	Asn	Leu	Asp	Ile	Ala	Pro	Ala	Ala	Asp	145	150	155	160
Gly	Tyr	Gly	Leu	Ala	Gly	Phe	Pro	Pro	Glu	His	Arg	Ala	Trp	Arg	Glu	165	170	175	
Glu	Pro	Trp	Ile	His	His	Ala	Pro	Pro	Gly	Cys	Gly	Asn	Ala	Pro	Arg	180	185	190	
Ser	Ser	Ile	Ser	Asn	Thr	Cys	Asp	Glu	Lys	Thr	Gln	Ser	Leu	Gly	Val	195	200	205	
Lys	Phe	Leu	Asp	Glu	Tyr	Gln	Ser	Lys	Val	Lys	Arg	Gln	Ile	Phe	Ser	210	215	220	
Gly	Tyr	Gln	Ser	Asp	Ile	Asp	Thr	His	Asn	Arg	Ile	Lys	Asp	Glu	Leu	225	230	235	240